

IN THE CLAIMS

Please amend the claims as follows:

Claims 1-22 (Cancelled)

Claim 23 (Previously Presented): A method for assessing the risk of vesnarinone-induced granulocytopenia comprising:

detecting in a subject in need thereof at least one polynucleotide polymorphism of the human insulin receptor substrate 2 gene in the polynucleotide sequence described by GenBank Accession No. AL162497 (version 20)(SEQ ID NO: 18), and

assessing the risk of vesnarinone-induced granulocytopenia by detecting the the presence of at least one polymorphism correlating with the risk of vesnarinone-induced granulocytopenia; wherein said at least one polymorphism comprises a polymorphism A29793G that is a T to C conversion at position 96,095 of SEQ ID NO: 18.

Claim 24 (Cancelled)

Claim 25 (Previously Presented): The method of claim 23, wherein the genetic polymorphism is detected through at least one technique selected from the group consisting of allele-specific oligonucleotide (ASO)-dot blot analysis, single nucleotide primer extension assay, PCR-single strand conformation polymorphism (SSCP) analysis, Invader assay, quantitative real-time PCR assay, and genetic polymorphism assay employing a mass spectrometer (mass array).

Claim 26 (Previously Presented): The method of claim 23, wherein the genetic polymorphism is detected through direct nucleotide sequencing.

Claim 27 (Previously Presented): The method of claim 23, wherein the genetic polymorphism is detected through PCR-restriction enzyme fragment length polymorphism (RFLP) analysis.

Claim 28 (Previously Presented): The method of claim 27, wherein the PCR-restriction enzyme fragment length polymorphism (RFLP) analysis is performed by use of the restriction enzyme *Afa* I for detecting T to C conversion at position 96,095 of SEQ ID NO: 18.

Claim 29 (Cancelled)

Claim 30 (Previously Presented): The method of claim 23, wherein said polymorphism is identified by a method employing a probe or primer selected from the group consisting of:

(a) an oligonucleotide having a sequence including a genetic polymorphism that is G to T conversion at position 130,474 of SEQ ID NO: 18;

(b) an oligonucleotide having a sequence including a genetic polymorphism that is an TA deletion at positions 128,398-128,399 of SEQ ID NO: 18;

(c) an oligonucleotide having a sequence including a gene polymorphism that is T to G conversion at position 127,051 of SEQ ID NO: 18;

(d) an oligonucleotide having a sequence including a gene polymorphism that is T to C conversion at position of 110,018 of SEQ ID NO: 18;

(e) an oligonucleotide having a sequence including a gene polymorphism that is T to C conversion at position 96,095 of SEQ ID NO: 18; and

(f) an oligonucleotide having a sequence including a genetic polymorphism that is G deletion between positions 94,356-94,357 of SEQ ID NO: 18.

Claim 31 (Cancelled)

Claim 32 (Previously Presented): The method of claim 23, wherein said polymorphism is identified by a method employing a probe or primer selected from the group consisting of:

- (a) an oligonucleotide having the sequence of SEQ ID NO: 3;
- (b) an oligonucleotide having the sequence of SEQ ID NO: 6;
- (c) an oligonucleotide having the sequence of SEQ ID NO: 9;
- (d) an oligonucleotide having the sequence of SEQ ID NO: 12; and
- (f) an oligonucleotide having the sequence of SEQ ID NO: 17.

Claim 33 (Previously Presented): The method of claim 32, comprising assessing the risk of vesnarinone-induced granulocytopenia before vesnarinone administration.

Claim 34 (Previously Presented): The method of claim 23, wherein said polymorphism is identified by a method employing a probe or primer having a sequence including a gene polymorphism that is T to C conversion at position 96,095 of SEQ ID NO: 18 and employing the restriction enzyme *Afa* I.

Claim 35 (Previously Presented): The method of claim 34, comprising assessing the risk of vesnarinone-induced granulocytopenia before vesnarinone administration.

Claim 36 (Cancelled)

Claim 37 (Currently Amended): The method of claim ~~[[36]]~~ 32, further comprising obtaining a cDNA or genomic DNA sample from said subject.